



SEQUENCE LISTING

<110> OLSON, ERIC
ARAI, AKIKO

<120> STARS - A MUSCLE-SPECIFIC ACTIN-BINDING PROTEIN

<130> MYOG:037US

<140> 10/644,659

<141> 2003-08-20

<150> 60/404,706

<151> 2002-08-20

<160> 15

<170> PatentIn Ver. 2.1

<210> 1

<211> 1146

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1146)

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ctc cgg aag ata cgc aca gcc acc ctg gtc atc agc ttg gcc cga ggt 96
Leu Arg Lys Ile Arg Thr Ala Thr Leu Val Ile Ser Leu Ala Arg Gly
20 25 30

tgg cag cag tgg gcg aat gag aac agc atc agg cag gcc cag gag cct 144
Trp Gln Gln Trp Ala Asn Glu Asn Ser Ile Arg Gln Ala Gln Glu Pro
35 40 45

aca ggc tgg ctg ccg gga ggg acc cag gac tca cct caa gct cct aaa 192
Thr Gly Trp Leu Pro Gly Gly Thr Gln Asp Ser Pro Gln Ala Pro Lys
50 55 60

cca atc aca ccc cct act tca cac cag aaa gct cag agt gcc cca aag 240
Pro Ile Thr Pro Pro Thr Ser His Gln Lys Ala Gln Ser Ala Pro Lys
65 70 75 80

tcg cca ccc cgc ctg cca gaa gga cat gga gat gga caa agc tca gag	288
Ser Pro Pro Arg Leu Pro Glu Gly His Gly Asp Gly Gln Ser Ser Glu	
85 90 95	
aaa gcc cct gag gtt tct cac atc aaa aag aaa gag gtg tcc aaa acg	336
Lys Ala Pro Glu Val Ser His Ile Lys Lys Lys Glu Val Ser Lys Thr	
100 105 110	
gtg gtc agc aag act tac gag aga gga ggg gac gtg agc cac ctc agc	384
Val Val Ser Lys Thr Tyr Glu Arg Gly Gly Asp Val Ser His Leu Ser	
115 120 125	
cac agg tac gag agg gat gct ggt gtg ctt gaa cct ggg cag cca gag	432
His Arg Tyr Glu Arg Asp Ala Gly Val Leu Glu Pro Gly Gln Pro Glu	
130 135 140	
aat gac att gac aga atc ctc cac agc cac ggc tcc cca acg cgg agg	480
Asn Asp Ile Asp Arg Ile Leu His Ser His Gly Ser Pro Thr Arg Arg	
145 150 155 160	
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Arg Lys Cys Ala Asn Leu Val Ser Glu Leu Thr Lys Gly Trp Arg Val	
165 170 175	
atg gag cag gag gag ccc aca tgg agg agt gac agc gta gac aca gag	576
Met Glu Gln Glu Glu Pro Thr Trp Arg Ser Asp Ser Val Asp Thr Glu	
180 185 190	
gac agc ggc tat gga gga gag gct gag gag agg ccc gag cag gat gga	624
Asp Ser Gly Tyr Gly Gly Glu Ala Glu Glu Arg Pro Glu Gln Asp Gly	
195 200 205	
gtg cag gtg gct gtg gtc agg atc aag cgc ccc ttg ccc tcc cag gta	672
Val Gln Val Ala Val Val Arg Ile Lys Arg Pro Leu Pro Ser Gln Val	
210 215 220	
aac aga ttt aca gag aaa ctc aac tgc aaa gcc caa cag aaa tat agc	720
Asn Arg Phe Thr Glu Lys Leu Asn Cys Lys Ala Gln Gln Lys Tyr Ser	
225 230 235 240	
cca gtg ggc aac ttg aaa ggg aga tgg cag cag tgg gct gat gaa cac	768
Pro Val Gly Asn Leu Lys Gly Arg Trp Gln Gln Trp Ala Asp Glu His	
245 250 255	
ata caa tcc cag aag ctc aat cct ttc agt gaa gag ttt gat tac gag	816
Ile Gln Ser Gln Lys Leu Asn Pro Phe Ser Glu Glu Phe Asp Tyr Glu	
260 265 270	

ctg gcc atg tcc acc cgc cta cac aaa gga gat gag ggc tat ggc cgc	864
Leu Ala Met Ser Thr Arg Leu His Lys Gly Asp Glu Gly Tyr Gly Arg	
275 280 285	
ccc aaa gaa gga acc aaa act gct gaa agg gcc aag cgt gct gag gag	912
Pro Lys Glu Gly Thr Lys Thr Ala Glu Arg Ala Lys Arg Ala Glu Glu	
290 295 300	
cac atc tac agg gaa atg atg gac atg tgc ttc att atc tgc aca atg	960
His Ile Tyr Arg Glu Met Met Asp Met Cys Phe Ile Ile Cys Thr Met	
305 310 315 320	
gct cgc cac aga cga gat ggc aag atc cag gtt act ttt gga gat ctc	1008
Ala Arg His Arg Arg Asp Gly Lys Ile Gln Val Thr Phe Gly Asp Leu	
325 330 335	
ttt gac aga tac gtt cgt att tca gat aaa gta gtg ggc att ctc atg	1056
Phe Asp Arg Tyr Val Arg Ile Ser Asp Lys Val Val Gly Ile Leu Met	
340 345 350	
cgt gcc agg aaa cat gga ctg gta gac ttt gaa gga gag atg cta tgg	1104
Arg Ala Arg Lys His Gly Leu Val Asp Phe Glu Gly Glu Met Leu Trp	
355 360 365	
caa ggc cga gat gac cat gtt gtg att acg cta ctc aag tga	1146
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<210> 2

<211> 381

<212> PRT

<213> Homo sapiens

<400> 2

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35 40 45	
Thr Gly Trp Leu Pro Gly Gly Thr Gln Asp Ser Pro Gln Ala Pro Lys	
50 55 60	
Pro Ile Thr Pro Pro Thr Ser His Gln Lys Ala Gln Ser Ala Pro Lys	
65 70 75 80	
Ser Pro Pro Arg Leu Pro Glu Gly His Gly Asp Gly Gln Ser Ser Glu	
85 90 95	

Lys	Ala	Pro	Glu	Val	Ser	His	Ile	Lys	Lys	Lys	Glu	Val	Ser	Lys	Thr	100	105	110
Val	Val	Ser	Lys	Thr	Tyr	Glu	Arg	Gly	Gly	Asp	Val	Ser	His	Leu	Ser	115	120	125
His	Arg	Tyr	Glu	Arg	Asp	Ala	Gly	Val	Leu	Glu	Pro	Gly	Gln	Pro	Glu	130	135	140
Asn	Asp	Ile	Asp	Arg	Ile	Leu	His	Ser	His	Gly	Ser	Pro	Thr	Arg	Arg	145	150	155
Arg	Lys	Cys	Ala	Asn	Leu	Val	Ser	Glu	Leu	Thr	Lys	Gly	Trp	Arg	Val	165	170	175
Met	Glu	Gln	Glu	Glu	Pro	Thr	Trp	Arg	Ser	Asp	Ser	Val	Asp	Thr	Glu	180	185	190
Asp	Ser	Gly	Tyr	Gly	Gly	Glu	Ala	Glu	Glu	Arg	Pro	Glu	Gln	Asp	Gly	195	200	205
Val	Gln	Val	Ala	Val	Val	Arg	Ile	Lys	Arg	Pro	Leu	Pro	Ser	Gln	Val	210	215	220
Asn	Arg	Phe	Thr	Glu	Lys	Leu	Asn	Cys	Lys	Ala	Gln	Gln	Lys	Tyr	Ser	225	230	235
Pro	Val	Gly	Asn	Leu	Lys	Gly	Arg	Trp	Gln	Gln	Trp	Ala	Asp	Glu	His	245	250	255
Ile	Gln	Ser	Gln	Lys	Leu	Asn	Pro	Phe	Ser	Glu	Glu	Phe	Asp	Tyr	Glu	260	265	270
Leu	Ala	Met	Ser	Thr	Arg	Leu	His	Lys	Gly	Asp	Glu	Gly	Tyr	Gly	Arg	275	280	285
Pro	Lys	Glu	Gly	Thr	Lys	Thr	Ala	Glu	Arg	Ala	Lys	Arg	Ala	Glu	Glu	290	295	300
His	Ile	Tyr	Arg	Glu	Met	Met	Asp	Met	Cys	Phe	Ile	Ile	Cys	Thr	Met	305	310	315
Ala	Arg	His	Arg	Arg	Asp	Gly	Lys	Ile	Gln	Val	Thr	Phe	Gly	Asp	Leu	325	330	335
Phe	Asp	Arg	Tyr	Val	Arg	Ile	Ser	Asp	Lys	Val	Val	Gly	Ile	Leu	Met	340	345	350
Arg	Ala	Arg	Lys	His	Gly	Leu	Val	Asp	Phe	Glu	Gly	Glu	Met	Leu	Trp	355	360	365
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<210> 3

<211> 1128

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1128)

<400> 3

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Leu Arg Lys Val Arg Thr Ala Thr Leu Val Ile Asn Leu Ala Arg Gly	
20 25 30	
tgg cag cag tgg gcg aat gag aac agt acc aaa cag gcc cag gag cct	144
Trp Gln Gln Trp Ala Asn Glu Asn Ser Thr Lys Gln Ala Gln Glu Pro	
35 40 45	
gca ggc tgg ctg ccg gga gca act cat gac gta cct aac gct cct aaa	192
Ala Gly Trp Leu Pro Gly Ala Thr His Asp Val Pro Asn Ala Pro Lys	
50 55 60	
gaa gcc ggt cct tac cag cat gcc ccc aaa act ctg tct cca aag cca	240
Glu Ala Gly Pro Tyr Gln His Ala Pro Lys Thr Leu Ser Pro Lys Pro	
65 70 75 80	
gat cga gac gga gag gga caa cac tca gaa gaa gcc acc gag gtc tcc	288
Asp Arg Asp Gly Glu Gly Gln His Ser Glu Glu Ala Thr Glu Val Ser	
85 90 95	
cac att aaa agg aaa gag gtg acc aga acg gtt gtc agc aag gct tat	336
His Ile Lys Arg Lys Glu Val Thr Arg Thr Val Val Ser Lys Ala Tyr	
100 105 110	
gag agg gga gga gat gtg aac tac ctg agc cac agg tat gag aat gat	384
Glu Arg Gly Gly Asp Val Asn Tyr Leu Ser His Arg Tyr Glu Asn Asp	
115 120 125	
ggt ggc gtg tct gaa gct att cag cca gag aat gac att gac aga atc	432
Gly Gly Val Ser Glu Ala Ile Gln Pro Glu Asn Asp Ile Asp Arg Ile	
130 135 140	
ctt ctt agt cac gac tcg cca aca cgg aga aga aaa tgc acc aac ctg	480
Leu Leu Ser His Asp Ser Pro Thr Arg Arg Arg Lys Cys Thr Asn Leu	
145 150 155 160	
gtg tct gag ctg acc aaa ggc tgg aaa gtg atg gaa cag gaa gag ccc	528
Val Ser Glu Leu Thr Lys Gly Trp Lys Val Met Glu Gln Glu Glu Pro	
165 170 175	
acg tgg aag agt gac agc gta gac aca gag gac agt ggc tac gga ggg	576
Thr Trp Lys Ser Asp Ser Val Asp Thr Glu Asp Ser Gly Tyr Gly Gly	
180 185 190	

gat atg gag gag agg cct gag caa gat gca gcg cct gtg gct cct gcc	624
Asp Met Glu Glu Arg Pro Glu Gln Asp Ala Ala Pro Val Ala Pro Ala	
195 200 205	
agg atc aaa cgc ccc ttg cac tcc cag gca aac agg tac tct gag cca	672
Arg Ile Lys Arg Pro Leu His Ser Gln Ala Asn Arg Tyr Ser Glu Pro	
210 215 220	
ctc aac tgt aag gcc cat cgg aaa tac agc caa gtg gac aac ttg aaa	720
Leu Asn Cys Lys Ala His Arg Lys Tyr Ser Gln Val Asp Asn Leu Lys	
225 230 235 240	
ggg agg tgg cag cag tgg gcc gat gaa cac gtc cag tcc cag aag ctc	768
Gly Arg Trp Gln Gln Trp Ala Asp Glu His Val Gln Ser Gln Lys Leu	
245 250 255	
aat ccc ttc agt gac gaa ttt gac tat gac cta gcc atg tcc act cgg	816
Asn Pro Phe Ser Asp Glu Phe Asp Tyr Asp Leu Ala Met Ser Thr Arg	
260 265 270	
ctc cac aag gga gac gag ggc tat ggc cgc ccc aaa gag gga agc aag	864
Leu His Lys Gly Asp Glu Gly Tyr Gly Arg Pro Lys Glu Gly Ser Lys	
275 280 285	
aca gct gaa agg gcc aag cga gcg gaa gag cac atc tat cgg gaa att	912
Thr Ala Glu Arg Ala Lys Arg Ala Glu Glu His Ile Tyr Arg Glu Ile	
290 295 300	
atg gaa ctg tgc ttt gtt atc cgc aca atg gct cgc cac aga cga gat	960
Met Glu Leu Cys Phe Val Ile Arg Thr Met Ala Arg His Arg Arg Asp	
305 310 315 320	
ggc aag atc cag gtt act ttc gga gaa ctc ttt gat cgc tat gtt cgc	1008
Gly Lys Ile Gln Val Thr Phe Gly Glu Leu Phe Asp Arg Tyr Val Arg	
325 330 335	
att tct gat aaa gtc gtg ggc atc ctc atg cgt gcc agg aaa cac gga	1056
Ile Ser Asp Lys Val Val Gly Ile Leu Met Arg Ala Arg Lys His Gly	
340 345 350	
ctg gtg cac ttt gaa gga gag atg cta tgg caa ggc cga gac gac cat	1104
Leu Val His Phe Glu Gly Glu Met Leu Trp Gln Gly Arg Asp Asp His	
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 <213> Mus musculus

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Trp	Gln	Gln	Trp	Ala	Asn	Glu	Asn	Ser	Thr	Lys	Gln	Ala	Gln	Glu	Pro
			35				40					45			
Ala	Gly	Trp	Leu	Pro	Gly	Ala	Thr	His	Asp	Val	Pro	Asn	Ala	Pro	Lys
	50					55					60				
Glu	Ala	Gly	Pro	Tyr	Gln	His	Ala	Pro	Lys	Thr	Leu	Ser	Pro	Lys	Pro
65					70					75				80	
Asp	Arg	Asp	Gly	Glu	Gly	Gln	His	Ser	Glu	Glu	Ala	Thr	Glu	Val	Ser
				85					90					95	
His	Ile	Lys	Arg	Lys	Glu	Val	Thr	Arg	Thr	Val	Val	Ser	Lys	Ala	Tyr
			100					105					110		
Glu	Arg	Gly	Gly	Asp	Val	Asn	Tyr	Leu	Ser	His	Arg	Tyr	Glu	Asn	Asp
	115						120					125			
Gly	Gly	Val	Ser	Glu	Ala	Ile	Gln	Pro	Glu	Asn	Asp	Ile	Asp	Arg	Ile
	130					135					140				
Leu	Leu	Ser	His	Asp	Ser	Pro	Thr	Arg	Arg	Arg	Lys	Cys	Thr	Asn	Leu
145					150					155					160
Val	Ser	Glu	Leu	Thr	Lys	Gly	Trp	Lys	Val	Met	Glu	Gln	Glu	Glu	Pro
			165						170				175		
Thr	Trp	Lys	Ser	Asp	Ser	Val	Asp	Thr	Glu	Asp	Ser	Gly	Tyr	Gly	Gly
			180					185					190		
Asp	Met	Glu	Glu	Arg	Pro	Glu	Gln	Asp	Ala	Ala	Pro	Val	Ala	Pro	Ala
	195						200					205			
Arg	Ile	Lys	Arg	Pro	Leu	His	Ser	Gln	Ala	Asn	Arg	Tyr	Ser	Glu	Pro
	210					215					220				
Leu	Asn	Cys	Lys	Ala	His	Arg	Lys	Tyr	Ser	Gln	Val	Asp	Asn	Leu	Lys
225				230						235				240	
Gly	Arg	Trp	Gln	Gln	Trp	Ala	Asp	Glu	His	Val	Gln	Ser	Gln	Lys	Leu
			245						250					255	
Asn	Pro	Phe	Ser	Asp	Glu	Phe	Asp	Tyr	Asp	Leu	Ala	Met	Ser	Thr	Arg
			260					265					270		
Leu	His	Lys	Gly	Asp	Glu	Gly	Tyr	Gly	Arg	Pro	Lys	Glu	Gly	Ser	Lys
	275						280					285			
Thr	Ala	Glu	Arg	Ala	Lys	Arg	Ala	Glu	Glu	His	Ile	Tyr	Arg	Glu	Ile
	290					295					300				
Met	Glu	Leu	Cys	Phe	Val	Ile	Arg	Thr	Met	Ala	Arg	His	Arg	Arg	Asp
305					310					315					320

Gly Lys Ile Gln Val Thr Phe Gly Glu Leu Phe Asp Arg Tyr Val Arg
 325 330 335
 Ile Ser Asp Lys Val Val Gly Ile Leu Met Arg Ala Arg Lys His Gly
 340 345 350
 Leu Val His Phe Glu Gly Glu Met Leu Trp Gln Gly Arg Asp Asp His
 355 360 365
 Val Val Ile Thr Leu Val Glu
 370 375

<210> 5
 <211> 612
 <212> DNA
 <213> Zebra Fish

<220>
 <221> modified_base
 <222> (497)
 <223> n = a, c, g or t/u

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 aatttcctag gaaatgaatc tcctactagg agacgctact gtgggggggaa agcaggggact 180
 tttgttaaag caatcggacg gaaagaggga aagtcgatgg gatcgcgaag tagcagtttg 240
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 gagaacgaac ccaagaaaca tgtcaacaga cacaagatta aagtgacaac gatgggtgac 360
 ctgcgagacc gctggcagcg tttcgctgaa gatcacatgg agggccagaa gctcaaccct 420
 ttcagtgaag agtttgacta tgatcatgca atggccactc gactccacaa aggcgacgcg 480
 ggctacggac gacccanaga aggatccaaa acagctcagc gagcagatcg agcccaaaag 540
 cacatctacc gcgagatgga ggagatgtgc ttcatcatac gagacatggg ccagcaggac 600
 aaacagggcc aa 612

<210> 6
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 <212> PRT
 <213> Zebra Fish

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 Phe Gly Lys Asp Leu Val Ser Val Ile Lys Glu Lys Ile Asn Thr Asn
 20 25 30
 Gln Leu Thr Thr Glu Asp Thr Lys Asn Phe Leu Gly Asn Glu Ser Pro

35	40	45	
Thr Arg Arg Arg Tyr Cys Gly Gly Lys Ala Gly Thr Phe Val Lys Ala			
50	55	60	
Ile Gly Arg Lys Glu Gly Lys Ser Met Gly Ser Arg Ser Ser Ser Leu			
65	70	75	80
Asp Ala Asp Asp Ser Gly Leu Gly Glu Glu Ala Ser Leu Ser Asp Asn			
85	90	95	
Ser Asp Leu Asn Glu Asn Glu Pro Lys Lys His Val Asn Arg His Lys			
100	105	110	
Ile Lys Val Thr Thr Met Gly Asp Leu Arg Ser Arg Trp Gln Arg Phe			
115	120	125	
Ala Glu Asp His Met Glu Gly Gln Lys Leu Asn Pro Phe Ser Glu Glu			
130	135	140	
Phe Asp Tyr Asp His Ala Met Ala Thr Arg Leu His Lys Gly Asp Ala			
145	150	155	160
Gly Tyr Gly Arg Pro Lys Lys Asp Pro Lys Gln Leu Ser Glu Gln Ile			
165	170	175	
Glu Pro Lys Ser Thr Ser Thr Ala Arg Trp Arg Arg Cys Ala Ser Ser			
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Tyr Glu Thr Trp Ala Ser Arg Thr Asn Arg Ala			
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 <212> DNA
 <213> Caenorhabditis elegans

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gaa atg gag cag aat gta gcg act cag agc aaa gat gat gtg tat tcc	96

Glu Met	Glu Gln	Asn Val	Ala Thr	Gln Ser	Lys Asp	Asp Val	Tyr Ser	
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aaa gat ttt act caa aag aaa atg gac aag tcc agt agc gaa tat gga								144
Lys Asp Phe Thr Gln Lys Lys Met Asp Lys Ser Ser Ser Glu Tyr Gly								
	35			40		45		
cgg cca aaa cca gga act ctt aca gag caa aga gct aaa aaa gct gcc								192
Arg Pro Lys Pro Gly Thr Leu Thr Glu Gln Arg Ala Lys Lys Ala Ala								
	50			55		60		
gcc cac gtt cac aga gaa atg cta aca tta tgt gaa gtt gtg gag gat								240
Ala His Val His Arg Glu Met Leu Thr Leu Cys Glu Val Val Glu Asp								
	65			70		75		80
tat ggt aaa caa gag aag gaa gga gat cca atc aga atc aca ttt gga								288
Tyr Gly Lys Gln Glu Lys Glu Gly Asp Pro Ile Arg Ile Thr Phe Gly								
		85			90		95	
aga ctt ttc aca att tat gtc aat att tct gat aag gta gtt gga acc								336
Arg Leu Phe Thr Ile Tyr Val Asn Ile Ser Asp Lys Val Val Gly Thr								
	100			105		110		
ctt ttg cga gct cgt aaa cac aaa atg ata gat ttt gaa gga gaa atg								384
Leu Leu Arg Ala Arg Lys His Lys Met Ile Asp Phe Glu Gly Glu Met								
	115			120		125		
tta ttt caa aag aga gat gat cat gtt att atc aca ctt tta ctc tct								432
Leu Phe Gln Lys Arg Asp Asp His Val Ile Ile Thr Leu Leu Leu Ser								
	130			135		140		
gga gca cag ctt aaa gag gct att cga gca cac gca gca gca aac cca								480
Gly Ala Gln Leu Lys Glu Ala Ile Arg Ala His Ala Ala Ala Asn Pro								
	145			150		155		160
aag gaa taa								489
Lys Glu								

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<211> 162

<212> PRT

<213> Caenorhabditis elegans

<400> 8

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Pro Phe Gly Glu Leu Phe Asn Val Ser Val Leu Phe Thr Ala Gly Ile
115 120 125

Phe Phe Glu Lys Pro Ser Lys Leu Val Thr Ser Thr Leu Gln Ile Tyr
130 135 140

Asn Tyr Ile Ser Asp Lys Val Val Gly Ile Leu Leu Arg Ala Arg Lys
145 150 155 160

His Lys Leu Val Asp Phe Glu Gly Glu Met Leu Tyr Gln Arg Arg Asp
165 170 175

Asp Asp Val Pro Val Phe Leu Leu Lys Pro Ile Lys Glu Ile Arg Ser
180 185 190

Glu Met Glu Ala Lys Ile Glu Asp Ile Lys Arg Ala Ala Ser Pro Ala
195 200 205

Pro Pro Gln Ser Thr Ser Val Leu Met Asp Arg Ser Ala His Glu Gln
210 215 220

Lys Leu Lys Ser Arg Thr Pro Ser Pro Ala Val Gly Lys Ser Ala Lys
225 230 235 240

Ser Lys Ser Ala Ser Pro Ala Pro Lys Ala Pro Val Pro Val Pro Ala
245 250 255

Pro Ala Ala Glu Val Thr Pro Val Ala Gly Pro Thr Thr Ser Ala Glu
260 265 270

Pro Ala Pro Val Ala Glu Ser Thr Met Ala Ala Val Pro Ala Pro Ser
275 280 285

Thr Glu Pro Thr Pro Ala Thr Ala Pro Ala Ser Ser Thr Val Glu Ile
290 295 300

Glu Pro Ala Lys Pro Glu Val Thr Glu Gln Ala Pro Val Ala Val Ile
305 310 315 320

Val Thr Glu Ala Pro Ser Thr Glu Glu Thr Thr Pro Thr Thr Ser Glu
325 330 335

Pro Gln Ala Glu Glu Ala Pro Ala Ala Val Ala Pro Ala Gly Pro Ala
340 345 350

Asp Asp Leu Pro Thr Ile Val Ile Glu Ala Thr Ala Glu Phe Val Arg
355 360 365

Thr Val Ser Val Glu Gln Leu Ala Pro Ser Pro Gly Thr Ala Ser Glu
370 375 380

Ser Ser Pro Asp Gln Ser Gln Ser Gln Pro Glu Ser Thr Pro Ala
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<210> 10
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<213> Artificial Sequence

<220>
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Primer

<400> 10
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<210> 11
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<212> DNA
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<220>
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Primer

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<210> 15
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<223> Description of Artificial Sequence: Synthetic
Primer

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